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## RAW SEQUENCE LISTING

DATE: 01/03/2002

PATENT APPLICATION: US/09/922,895

TIME: 15:28:15

Input Set : N:\Crf3\RULE60\09922895.raw

Output Set: N:\CRF3\01032002\I922895.raw

## SEQUENCE LISTING

**ENTERED**

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: DAUGHERTY, BRUCE L.  
 6 DEMARTINO, JULIE A.  
 7 SICILIANO, SALVATORE J.  
 8 SPRINGER, MARTIN J.

10 (ii) TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR

12 (iii) NUMBER OF SEQUENCES: 4

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Merck & Co., Inc.  
 16 (B) STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
 17 (C) CITY: Rahway  
 18 (D) STATE: NJ  
 19 (E) COUNTRY: USA  
 20 (F) ZIP: 07065-0900

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Diskette  
 24 (B) COMPUTER: IBM Compatible  
 25 (C) OPERATING SYSTEM: DOS  
 26 (D) SOFTWARE: FastSEQ for Windows Version 2.0

28 (vi) CURRENT APPLICATION DATA:

C--&gt; 29 (A) APPLICATION NUMBER: US/09/922,895

C--&gt; 30 (B) FILING DATE: 06-Aug-2001

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 08/847,296

35 (B) FILING DATE:

37 (A) APPLICATION NUMBER: 60/017,113

38 (B) FILING DATE: 26-APR-1996

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Thies, J. Eric  
 43 (B) REGISTRATION NUMBER: 35,382  
 44 (C) REFERENCE/DOCKET NUMBER: 19634Y

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: 908-594-3904  
 48 (B) TELEFAX: 908-594-4720  
 49 (C) TELEX:

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 355 amino acids  
 56 (B) TYPE: amino acid  
 57 (C) STRANDEDNESS: single  
 58 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

64 Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr  
 65 1 5 10 15

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66 Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
67      20                      25                      30
68 Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
69      35                      40                      45
70 Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
71      50                      55                      60
72 Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
73      65                      70                      75                      80
74 Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
75      85                      90                      95
76 His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
77      100                     105                     110
78 Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
79      115                     120                     125
80 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
81      130                     135                     140
82 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
83      145                     150                     155                     160
84 Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
85      165                     170                     175
86 Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
87      180                     185                     190
88 Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
89      195                     200                     205
90 Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
91      210                     215                     220
92 Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
93      225                     230                     235                     240
94 Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
95      245                     250                     255
96 Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
97      260                     265                     270
98 Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
99      275                     280                     285
100 Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
101      290                     295                     300
102 Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
103      305                     310                     315                     320
104 Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
105      325                     330                     335
106 Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
107      340                     345                     350
108 Ile Val Phe
109      355

```

111 (2) INFORMATION FOR SEQ ID NO: 2:

113 (i) SEQUENCE CHARACTERISTICS:

114 (A) LENGTH: 1065 base pairs

115 (B) TYPE: nucleic acid

116 (C) STRANDEDNESS: single

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117         (D) TOPOLOGY: linear
119     (ii) MOLECULE TYPE: cDNA
121     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
123 ATGACAACCT CACTAGATAC AGTTGAGACC TTTGGTACCA CATCCTACTA TGATGACGTG      60
124 GGCCTGCTCT GTGAAAAAGC TGATACCAGA GCACTGATGG CCCAGTTTGT GCCCCCCTG      120
125 TACTCCCTGG TGTTCACTGT GGGCCTCTTG GGCAATGTGG TGGTGGTGAT GATCCTCATA      180
126 AAATACAGGA GGCTCCGAAT TATGACCAAC ATCTACCTGC TCAACCTGGC CATTTTCGGAC      240
127 CTGCTCTTCC TCGTCAACCT TCCATTCTGG ATCCACTATG TCAGGGGGCA TAACTGGGTT      300
128 TTTGGCCATG GCATGTGTAA GCTCCTCTCA GGGTTTTATC ACACAGGCTT GTACAGCGAG      360
129 ATCTTTTTCA TAATCCTGCT GACAATCGAC AGGTACCTGG CCATTGTCCA TGCTGTGTTT      420
130 GCCCTTCGAG CCCGGACTGT CACTTTTGGT GTCATCACCA GCATCGTCAC CTGGGGCCTG      480
131 GCAGTGCTAG CAGCTCTTCC TGAATTTATC TTCTATGAGA CTGAAGAGTT GTTTGAAGAG      540
132 ACTCTTTGCA GTGCTCTTTA CCCAGAGGAT ACAGTATATA GCTGGAGGCA TTTCCACACT      600
133 CTGAGAATGA CCATCTTCTG TCTCGTTCTC CCTCTGCTCG TTATGGCCAT CTGCTACACA      660
134 GGAATCATCA AAACGCTGCT GAGGTGCCCC AGTAAAAAAA AGTACAAGGC CATCCGGCTC      720
135 ATTTTTGTCA TCATGGCGGT GTTTTTCATT TTCTGGACAC CCTACAATGT GGCTATCCTT      780
136 CTCTCTTCTT ATCAATCCAT CTTATTTGGA AATGACTGTG AGCGGAGCAA GCATCTGGAC      840
137 CTGGTCATGC TGGTGACAGA GGTGATCGCC TACTCCCACT GCTGCATGAA CCCGGTGATC      900
138 TACGCCTTTG TTGGAGAGAG GTTCCGGAAG TACCTGCGCC ACTTCTTCCA CAGGCACTTG      960
139 CTCATGCACC TGGGCAGATA CATCCCATTG CTTCTAGTGA AGAAGCTGGA AAGAACCAGC     1020
140 TCTGTCTCTC CATCCACAGC AGAGCCGGAA CTCTCTATTG TGTTT                      1065
142 (2) INFORMATION FOR SEQ ID NO: 3:
144     (i) SEQUENCE CHARACTERISTICS:
145         (A) LENGTH: 3586 base pairs
146         (B) TYPE: nucleic acid
147         (C) STRANDEDNESS: single
148         (D) TOPOLOGY: linear
150     (ii) MOLECULE TYPE: cDNA
152     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
154 GGATCCCTAC CTTCCCCATC AGAGCTAGGG GGCATGGAGC GCTCTCTGCT AAGATGGGGA      60
155 CCCCCAAGGA ATGTCTCCCT GTGGGGCACT TCCTTACCAG ATGGGATGGC CAGTGCGGTT      120
156 AAGTTGGTGG TCAGGCAGAA AAAAAAGATC TAGTTTGTAC TCTTGAGAGT TCCTCGGTTT      180
157 GTTCATGGCA TGGGCAGGGA GTCAAGGAGC AGCAGCCTTG CCTCAGTGCC TACCAGTGCA      240
158 GGAAAAGGTG CATAGCCTGG GCCAGGGCCA GGGCCCTGGT GGAGGCGTAG TGGTAACAGA      300
159 GAGGGCTCTC CATTCCAGCC CAAGGAAGAC TAAGAATGAA TACCTCATGA GTATATTAGC      360
160 TACAAACCAC CACAGCAGGT TCCAGAAAAA GGCTCAGCGT TGGAAACCAGG TCACCCCCAC      420
161 TCAGCAGACA CCAGTCATAT AAATCAAGGA CCAACAGGAG ACAGGAACAC CCCCTTCCCA      480
162 CTCTGCCCCA TGTCTCAAGT TGTAGTGGCC CTTCTCTCCAG ATCTCTGCCA CCATCTTAGA      540
163 AAGGAACACT GAAAGAAGAA ACTGAAATTA TAAGCTGACA GCATAAAGAG GATGAGTAAA      600
164 ACCTAAAATC ATTGTTTACA TGAATGAATC AAGAGAAGTT TAAACCACTT TGGACTAAAA      660
165 TGTGTGAATC CTTTTTCTTG CTATCCAGCA GATGAGAAGC TGGTAACAGA GACCACAATA      720
166 GTTTGGAGAC TAAAGAATCA TTGCACATTT CACTGCTGAG TTGTATTGTG AGTAATTTTA      780
167 GTTGACCTCA CTTTGTAATC CTTGCACACG GGGCAATCCA ATATCTGCAC AAGAGATATG      840
168 TTAACCAAGT GTAAATGCTG CATGAGGAGA TTGGGTGATT TTTACTTTTCG TTTTGTGCT      900
169 CTTCTTTCTT ATTGTTCTTA CTTATTTACG ATTACCCTAT CGTTTTCCCA AAATGTAAAA      960
170 GGCCATTTTG AAAGCCTAAT TCAAACCTCT TCACTATTTT GTATCTAAGT ATTCACCTTG     1020
171 ATTGAGACTG GGTAGACAGG TGAAAACCAT ATCAGGTTTT TAATTTTTTA ATTTTAAATT     1080
172 ATTTATTTAT TTATTTATTT TTTGAGATGG AGTCTGGCTG TCGCCCAGGC TGGAGTGCAG     1140
173 CGGCGTGATC ACAGTTCACT GCAGCCTCAA CCTTCTAGGC TCAAGGGATT CTCCCACCTC     1200

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174 AGCCCCCAA GTAGTTGGGA CCACACGTAT GCGCCACCAT GCCTGGCTAA TTTCTTATTT 1260
175 TTTTGTAGAG ATAGGATCTC ACTATATTGT CCAGGCTGGT CTTGAATTCC TGGGCTCAGG 1320
176 TGAGCCTCCC ACCTGGGCGT CCCAAAGTAC TGGGATTACA GGCATGAGCC AAGGTCCCCT 1380
177 GCCCATATGA GATTTTCTGT CTCTGATCCC ATGCAGCTAG TAATCAAGGA CTTGGCTGCT 1440
178 GACTCTGGAG GACCTGCACT CTTTCTTGAG CTGTGAACTT CAGTGCTAAA AGCTCATAGG 1500
179 CAGCCCTGAA ACCCAAACCA AAAGGTTCTA TGGTTTATCA TCCTGATCAT GTTGATTTTA 1560
180 TAGAAATAAC ACATGAATTA AAGACACTAC CCTCAAACCTG AGCAAAACTT AAGTAATTTT 1620
181 TTTAAAGTTT GACCTGTTTT TAAATCACTC TTGGAGAAAA AGGAAAATAA ATACAAATAA 1680
182 TTAACGGTGA ATACAGGCTA CTATACCTTT GTTCTCCAGA ATTAGCAGTT CTGTTCTTTT 1740
183 CTTGCTTTAG ATGCTGAAGT GCAGAAGGAC ACTCTGTGAT TGTACGTGTG TAACTGACAA 1800
184 AATGTGTATT TTTTTTCTCA GCTGCTATGG ATTGGATTAT GCTATTATGA ATAAGAATGC 1860
185 TGATGGGAGC ACACACAAAC CATTTGTTCC TCAGTCCATT TTCCTCCTCA AAAGCCTGGA 1920
186 ATGTGCCATT GATCAGTGGG AGATGTACCT GGACAGACCC ATGAAAAGAG ATCAACAAGT 1980
187 TCCACCCAAG GGACCTATT TTTCTAATT TCATTTGAAA TGGCTTCTAA TTGTCCTTCT 2040
188 TTCATTCTTG CTTCTACCA GTTTTACAGC TTTTCTGGT TTCAAATGTG AACTCACATA 2100
189 CACTCTCATT TTTCTCATC ACAACCCCAA GTGACCCAAT GGTCCTCACT TTCGATATAA 2160
190 GTAAAGGAGG CTCTGCATTA AGGGCTTGTC CAAGGCACGC AGCTGAGAGG CGCTAGGACT 2220
191 GGCTCCATT CCATCTCTAT TCTCACTGAC TTTGACTACC CAGAACCCCA ACATGTGGGG 2280
192 CCTCAGTATT CGATCAATTA TTCTATTAG AAGCAAAAC AATTCCCGC ATTGGCCCA 2340
193 GTTATTAAAG ATTTCTCAGA TTTACCTTGA GAAATGCCCA TCGGCCTGTA TATTACATC 2400
194 TTCACCTTG TCCCTTCTC CTAGAAAGGA GAAAGTCAGT TGGATGCCCT CTGAGGAAct 2460
195 AGTGCATGGC TTAAGTGTCC TTCCATGACT CCTGCCTTAT CTGTTTTCTA TTTTCTCCT 2520
196 TTTCCACCGA AGTCTATAAT CTCAAGAAAA GCAGGCACTG GCCTTAGGGC TCCTGGCCTA 2580
197 AGAAATATCA AGTCCAGTGA GAAATCCCAT TGACTGACCC CTCCTGCTTA CCCCTTTGTG 2640
198 ATGGAGAAGC TCCAGGGGT TTGCTTTTTG CATGTTACCA GGCCTAACTC AGCATCACCA 2700
199 GGGCAAGAA AAGGAAAGTA ACCTAACTA ATGCTGCTTA TAATTGTAAT TATTGTAATA 2760
200 GTTAATTACT GTGATTGTAC ATGTGTAACA GACAAAATGT GTATTTTTTT CACAGCTGCT 2820
201 GTGGATTGGA TTATGCCATT TGGAATAAGA ATGCTGTAA GAGCACACAA GCCAGGTTCC 2880
202 TCAAGTCCGT AGCAAAATTT TCAAAAGTTA AATTTAAAAA TCACTACATT TGAATCTAGT 2940
203 GACAGGAGAA ATGGACATGG ATAGAGACTA AAGATCTAGC CCAAATTTTA TATTTACTTG 3000
204 TTAGAGGATT TTGAACAAAT TACTAAATTT CTTCAAGGTT CAATTTCCCC ATTAACATA 3060
205 ATGAATGTCT CATCATTATG GGGCCCTGGA GAAGCATAAT TACTTGTAAT TGAATAATC 3120
206 ATTGTTATTA TTATTATACA TATTTTGCTT TTAAATGGAT AAGGATTTTT AAGGTATATG 3180
207 TAACTGTAA AACATAAAAT GCAAAATGCC GTAAGAGACA GTAGTAATAA TAATGATTAT 3240
208 TATATTGTTA TCATTATCTA GCCTGTTTTT TCCTGTTGTG TATTTCTTCC TTTAAATGCT 3300
209 TACAGAAATC TGTATCCCCA TTCTTACCA CCACCCACA ACATTTCTGC TTCTTTTCCC 3360
210 ATGCCGGTCA TGCTAACTTT GAAAGCTTCA GCTCTTTCCT TCCTCAATCC TTCTCCTGGC 3420
211 ACCTCTGATA TGCCTTTTGA AATTCATGTT AAAGAATCCC TAGGCTGCTA TCACATGTGG 3480
212 CATCTTTGTT GAGTACATGA ATAAATCAAC TGGTGTGTTT TACGAAGGAT GATTATGCTT 3540
213 CATTGTGGGA TTGTATTTTT CTTCTTCTAT CACAGGGAGA AGTGAA 3586

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215 (2) INFORMATION FOR SEQ ID NO: 4:

217 (i) SEQUENCE CHARACTERISTICS:

218 (A) LENGTH: 448 base pairs

219 (B) TYPE: nucleic acid

220 (C) STRANDEDNESS: single

221 (D) TOPOLOGY: linear

223 (ii) MOLECULE TYPE: cDNA

225 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

227 TAGGTCAGAT GCAGAAATT GCCTAAAGAG GAAGGACCAA GGAGATGAAG CAAACACATT 60

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228	AAGCCTTCCA	CACTCACCTC	TAAAACAGTC	CTTCAAACCTT	CCAGTGCAAC	ACTGAAGCTC	120
229	TTGAAGACAC	TGAAATATAC	ACACAGCAGT	AGCAGTAGAT	GCATGTACCC	TAAGGTCATT	180
230	ACCACAGGCC	AGGGGCTGGG	CAGCGTACTC	ATCATCAACC	CTAAAAAGCA	GAGCTTTGCT	240
231	TCTCTCTCTA	AAATGAGTTA	CCTACATTTT	AATGCACCTG	AATGTTAGAT	AGTTACTATA	300
232	TGCCGCTACA	AAAAGGTAAA	ACTTTTTTATA	TTTTATACAT	TAACTTCAGC	CAGCTATTGA	360
233	TATAAATAAA	ACATTTTCAC	ACAATACAAT	AAGTTAACTA	TTTTATTTTC	TAATGTGCCT	420
234	AGTTCTTTCC	CTGCTTAATG	AAAAGCTT				448

VERIFICATION SUMMARY

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]